

Additionally, the amino acid valine was inadvertently inserted (*i.e.*, a typographical error) at position 341 of SEQ ID NO:2 in applicants' previous Preliminary Amendments (filed 07 October 1999 and 03 January 2000) made in response to an invitation to correct defects in the originally-filed Sequence Listing for the underlying U. S. parent application (Serial No. 09/234,208). This inadvertent insertion was perpetuated in the present CIP filing.

Accordingly, applicants now delete this valine residue, resulting in a 419 amino acid sequence for SEQ ID NO:2 as it was listed in applicants' original Sequence Listing for the underlying U. S. parent application (Serial No. 09/234,208). Support for this amendment is found in the originally-filed Sequence Listing of the parent, and throughout the current and parent specification and claims, which refer to an amino acid sequence (for SEQ ID NO:2) of up to about 419 amino acids.

The present inventor listing conforms to the true inventors as reflected in our Petition to Correct Inventorship which will be submitted under separate cover.

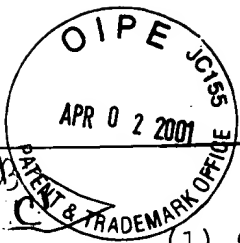
Applicants assert that the presently submitted Sequence Listing not only conforms with that of the underlying U. S. parent application (Serial No. 09/234,208), but also with the requirements of C.F.R. 1.821-1.825, and brings applicants' current specification into conformity with the presently-submitted Sequence Listing. No new matter has been added.

Applicants, in concert with this Preliminary Amendment, have responded to the above-identified NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES.

Respectfully submitted,

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

01 5 (i) APPLICANTS: Clinton, Gail M., Adam Evans and William D. Henner

(ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS

10 (iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIS WRIGHT TREMAINE

(B) STREET: 1501 Fourth Avenue, 2600 Century Square

15 (C) CITY: Seattle

(D) STATE: Washington

(E) COUNTRY: U.S.A.

(F) ZIP: 98101

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: PC compatible

(C) OPERATING SYSTEM: Windows 95

25 (D) SOFTWARE: Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/506,079

(B) FILING DATE: 16 February 2000

30 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Davison, Barry L.

(B) REGISTRATION NUMBER: 47,309

35 (C) REFERENCE/DOCKET NUMBER: 49321-16

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206 628 7621

(B) TELEFAX: 206 628 7699

40 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 79

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HER-2 ECD antagonist

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro Xaa
5 10 15
Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
20 25 30
Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
35 40 45
10 Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val Gly Arg Gly Xaa
50 55 60
Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg Tyr Glu Gly
65 70 75

15

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419

20

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
5 10 15
Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys
20 25 30
30 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
35 40 45
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
50 55 60
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
35 65 70 75 80
Gln Gly Tyr Val Leu Cys Ala His Asn Gln Val Arg Gln Val Pro Leu
85 90 95
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
100 105 110
40 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Agn Agn Thr Thr Pro
115 120 125
Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
130 135 140
Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
45 145 150 155 160
Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
165 170 175

	Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys
				180					185					190		
	His	Pro	Cys	Ser	Pro	Cys	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser
			195					200					205			
5	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys
		210					215					220				
	Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys
	225					230					235					240
	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu
10					245					250					255	
	His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val
				260				265						270		
	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Cys	Pro	Asn	Pro	Glu	Gly	Arg
			275					280					285			
15	Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Lys	Leu
		290					295					300				
	Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln
	305					310					315					320
	Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys
20					325					330					335	
	Pro	Cys	Ala	Arg	Gly	Xaa	His	Ser	Xaa	Xaa	Pro	Arg	Pro	Ala	Ala	Val
				340					345					350		
	Pro	Val	Pro	Xaa	Arg	Xaa	Gln	Pro	Xaa	Pro	Ala	His	Pro	Val	Leu	Ser
			355					360					365			
25	Phe	Leu	Arg	Pro	Ser	Trp	Asp	Xaa	Val	Ser	Ala	Phe	Tyr	Ser	Leu	Pro
		370					375					380				
	Leu	Ala	Pro	Leu	Asp	Pro	Thr	Ser	Val	Xaa	Ile	Ser	Pro	Val	Ser	Val
	385					390				395						400
	Gly	Arg	Gly	Xaa	Asp	Pro	Asp	Ala	His	Val	Ala	Val	Xaa	Leu	Ser	Arg
30					405					410					415	
	Tyr	Glu	Gly													

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGAGCACCAT GGAGCTGGC 19

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22
 (B) TYPE: nucleic acid
5 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: oligonucleotide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

10 TCCGGCAGAA ATGCCAGGCT CC 22

(2) INFORMATION FOR SEQ ID NO:5:
 (i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 22
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: oligonucleotide
20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACACAGCGG TGTGAGAAGT GC 22

25 (2) INFORMATION FOR SEQ ID NO:6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: oligonucleotide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35 ATACCGGAC AGGTCAACAG C 21

(2) INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: oligonucleotide
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGGTACC CACTCACTGC 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCACACTGG CACGTCCAGA CC 22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCACGGATCC ATAGCAGACT GAGGAGG 27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGT WCC CAC TCA CYG CYC CCG AGG CCA GCT GCA GTT CCT GTC CCT	45
Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro	
5 10 15	

CWG CGC ATR CAG CCT GNC CCA GCC CAC CCT GTC CTA TCC TTC CTC	90
Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu	
20 25 30	

AGA CCC TCT TGG GAC MTA GTC TCT GCC TTC TAC TCT CTA CCC CTG	135
Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu	
35 40 45	

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GCC	CCC	CTC	AGC	CCT	ACA	AGT	GTC	CST	ATA	TCC	CCT	GTC	AGT	GTG	180
Ala	Pro	Leu	Ser	Pro	Thr	Ser	Val	Xaa	Ile	Ser	Pro	Val	Ser	Val	
				50					55					60	

5

GGG	AGG	GGC	CYG	GAC	CCT	GAT	GCT	CAT	GTG	GCT	GTT	SAC	CTG	TCC	225
Gly	Arg	Gly	Xaa	Asp	Pro	Asp	Ala	His	Val	Ala	Val	Xaa	Leu	Ser	
				65					70					75	

10

CGG	TAT	GAA	GGC	TGA											240
Arg	Tyr	Glu	Gly												